

#2



OIPE

RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/10/047,825

TIME: 17:14:15

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\02052002\J047825.raw

ENTERED

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4 <110> APPLICANT: Duvick, Jon
5     Maddox, Joyce
6     Navarro Acevedo, Pedro
7     Simmons, Carl R.
9 <120> TITLE OF INVENTION: Maize Peroxidase Genes and Their Use for
10    Improving Plant Disease Resistance and Stalk Strength
13 <130> FILE REFERENCE: 35718/242052
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/047,825
C--> 15 <141> CURRENT FILING DATE: 2002-01-16
15 <150> PRIOR APPLICATION NUMBER: US 60/262,595
16 <151> PRIOR FILING DATE: 2001-01-18
18 <160> NUMBER OF SEQ ID NOS: 37
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 831
24 <212> TYPE: DNA
25 <213> ORGANISM: Zea mays
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (57)...(716)
31 <400> SEQUENCE: 1
32 aattcggcac gaggaataat tagttagttg ccttacctga tcagtcacatca ccatgc atg 59
33                                     Met
34                                     1
36 agc tgc tgc atg cag ggt ggc ggc ccg gcg tac aag ttg cca ctg ggc 107
37 Ser Cys Cys Met Gln Gly Gly Gly Pro Ala Tyr Lys Leu Pro Leu Gly
38         5                10                15
40 agg cgc gac ggg ctg gcg ccg gca tcg aac gcc gcc gtc cta gcg gcg 155
41 Arg Arg Asp Gly Leu Ala Pro Ala Ser Asn Ala Ala Val Leu Ala Ala
42         20                25                30
44 ctc cca ccg ccg acg tcc aag gtg ccg acg ctg ctg tcc ttc ctg gcg 203
45 Leu Pro Pro Pro Thr Ser Lys Val Pro Thr Leu Leu Ser Phe Leu Ala
46         35                40                45
48 aag atc aac ctg gac gtg acg gac ctg gtg gcg ctg tcg ggc ggc cac 251
49 Lys Ile Asn Leu Asp Val Thr Asp Leu Val Ala Leu Ser Gly Gly His
50 50                55                60                65
52 acg gtg ggc atc gcg cac tgc ggc tcc ttc gac aac cgg ctg ttc ccg 299
53 Thr Val Gly Ile Ala His Cys Gly Ser Phe Asp Asn Arg Leu Phe Pro
54         70                75                80
56 acg cag gac ccg acg ctg aac aag ttc ttc gcg ggc cag ctg tac ccg 347
57 Thr Gln Asp Pro Thr Leu Asn Lys Phe Phe Ala Gly Gln Leu Tyr Arg
58         85                90                95
60 acc tgc ccg acc aac gcg acg gtc aac acg acg gcc aac gac gtc cgc 395

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61 Thr Cys Pro Thr Asn Ala Thr Val Asn Thr Thr Ala Asn Asp Val Arg
62      100      105      110
64 acg ccc aac gcc ttc gac aac aag tac tac gtg gac ctg ctc aac cgg 443
65 Thr Pro Asn Ala Phe Asp Asn Lys Tyr Tyr Val Asp Leu Leu Asn Arg
66      115      120      125
68 gag ggc ctc ttc acg tcg gac cag gac ctg ctg acc aac gcc acc acg 491
69 Glu Gly Leu Phe Thr Ser Asp Gln Asp Leu Leu Thr Asn Ala Thr Thr
70 130      135      140      145
72 cgc ccc atc gtc acg cgc ttc gcc gtc gac cag gac gcc ttc ttc gac 539
73 Arg Pro Ile Val Thr Arg Phe Ala Val Asp Gln Asp Ala Phe Phe Asp
74      150      155      160
76 cag ttc gtc tac tcc tac gtc aag atg ggg cag gtc aac gtg ctc acg 587
77 Gln Phe Val Tyr Ser Tyr Val Lys Met Gly Gln Val Asn Val Leu Thr
78      165      170      175
80 ggc tcc cag gga cag gtc cgc gcc aac tgc tcc gcg cgc aac ggc gcc 635
81 Gly Ser Gln Gly Gln Val Arg Ala Asn Cys Ser Ala Arg Asn Gly Ala
82      180      185      190
84 gct gct ggt gac agt gac ctg ccg tgg tcg tcc gtc gtc atc gag aca 683
85 Ala Ala Gly Asp Ser Asp Leu Pro Trp Ser Ser Val Val Ile Glu Thr
86      195      200      205
88 gtc gcc gac gcc gcc ggt agc ctc gtg ctc tag ataataagca aataagtagt 736
89 Val Ala Asp Ala Ala Gly Ser Leu Val Leu *
90 210      215
92 ttgaagcttt cttcgcatgc atgttgcaac aaataagcag ctagtagcgt tgggaataaaa 796
93 gcagctagta gcgatcaaaaa aaaaaaaaaa aaaaa 831
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 219
97 <212> TYPE: PRT
98 <213> ORGANISM: Zea mays
100 <400> SEQUENCE: 2
101 Met Ser Cys Cys Met Gln Gly Gly Gly Pro Ala Tyr Lys Leu Pro Leu
102 1      5      10      15
103 Gly Arg Arg Asp Gly Leu Ala Pro Ala Ser Asn Ala Ala Val Leu Ala
104      20      25      30
105 Ala Leu Pro Pro Pro Thr Ser Lys Val Pro Thr Leu Leu Ser Phe Leu
106      35      40      45
107 Ala Lys Ile Asn Leu Asp Val Thr Asp Leu Val Ala Leu Ser Gly Gly
108      50      55      60
109 His Thr Val Gly Ile Ala His Cys Gly Ser Phe Asp Asn Arg Leu Phe
110 65      70      75      80
111 Pro Thr Gln Asp Pro Thr Leu Asn Lys Phe Phe Ala Gly Gln Leu Tyr
112      85      90      95
113 Arg Thr Cys Pro Thr Asn Ala Thr Val Asn Thr Thr Ala Asn Asp Val
114      100      105      110
115 Arg Thr Pro Asn Ala Phe Asp Asn Lys Tyr Tyr Val Asp Leu Leu Asn
116      115      120      125
117 Arg Glu Gly Leu Phe Thr Ser Asp Gln Asp Leu Leu Thr Asn Ala Thr
118      130      135      140
119 Thr Arg Pro Ile Val Thr Arg Phe Ala Val Asp Gln Asp Ala Phe Phe

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120 145          150          155          160
121 Asp Gln Phe Val Tyr Ser Tyr Val Lys Met Gly Gln Val Asn Val Leu
122          165          170          175
123 Thr Gly Ser Gln Gly Gln Val Arg Ala Asn Cys Ser Ala Arg Asn Gly
124          180          185          190
125 Ala Ala Ala Gly Asp Ser Asp Leu Pro Trp Ser Ser Val Val Ile Glu
126          195          200          205
127 Thr Val Ala Asp Ala Ala Gly Ser Leu Val Leu
128          210          215
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 1354
133 <212> TYPE: DNA
134 <213> ORGANISM: Zea mays
136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (67)...(1008)
140 <400> SEQUENCE: 3
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142 cttgcc atg gcg tct ccc acc ttg atg caa tgc ctg gtc gcc gtt tcc 108
143      Met Ala Ser Pro Thr Leu Met Gln Cys Leu Val Ala Val Ser
144      1          5          10
146 ctc ctc tcc tgt gtc gcc cac gca cag ctc tcg ccc acg ttc tat gcg 156
147 Leu Leu Ser Cys Val Ala His Ala Gln Leu Ser Pro Thr Phe Tyr Ala
148 15          20          25          30
150 tcc tcc tgc ccc aac ctg cag agc atc gtt cgg gcg gcg atg acc cag 204
151 Ser Ser Cys Pro Asn Leu Gln Ser Ile Val Arg Ala Ala Met Thr Gln
152          35          40          45
154 gcc gtc gca agt gag cag agg atg ggc gcc tct ctg ctc agg ctc ttc 252
155 Ala Val Ala Ser Glu Gln Arg Met Gly Ala Ser Leu Leu Arg Leu Phe
156          50          55          60
158 ttc cac gac tgc ttc gtt caa ggc tgc gac gga tcg atc ctt ctc gac 300
159 Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly Ser Ile Leu Leu Asp
160          65          70          75
162 gcc gga ggg gag aag acc gcc ggg ccg aac ctg aac tcg gtg cgc ggc 348
163 Ala Gly Gly Glu Lys Thr Ala Gly Pro Asn Leu Asn Ser Val Arg Gly
164          80          85          90
166 ttt gag gtc atc gac acc atc aag cgg aac gtc gag gcc gcg tgc ccc 396
167 Phe Glu Val Ile Asp Thr Ile Lys Arg Asn Val Glu Ala Ala Cys Pro
168 95          100          105          110
170 ggc gtc gtg tcg tgc gcc gac atc ctc gcg ctt gcc gcg cgc gac gga 444
171 Gly Val Val Ser Cys Ala Asp Ile Leu Ala Leu Ala Ala Arg Asp Gly
172          115          120          125
174 acc aac ctt ctc ggc ggg ccg acc tgg agc gtg ccg ctc ggg cgg cgg 492
175 Thr Asn Leu Leu Gly Gly Pro Thr Trp Ser Val Pro Leu Gly Arg Arg
176          130          135          140
178 gac tcg acg acg gcc agc gcc tcg ctc gcc aac agc aac ccc ccg ccc 540
179 Asp Ser Thr Thr Ala Ser Ala Ser Leu Ala Asn Ser Asn Pro Pro Pro
180          145          150          155
182 ccg acg gcc agc ctc ggc acg ctc atc tcc ctg ttc ggc agg cag ggc 588

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183 Pro Thr Ala Ser Leu Gly Thr Leu Ile Ser Leu Phe Gly Arg Gln Gly
184      160      165      170
186 ctg tcg ccg cgc gac atg acg gcg ctg tcg ggc gcg cac acc atc ggg 636
187 Leu Ser Pro Arg Asp Met Thr Ala Leu Ser Gly Ala His Thr Ile Gly
188 175      180      185      190
190 cag gcc cgg tgc acc acc ttc cgc ggc cgc atc tac ggc gac acc gac 684
191 Gln Ala Arg Cys Thr Thr Phe Arg Gly Arg Ile Tyr Gly Asp Thr Asp
192      195      200      205
194 atc aac gcc tcc ttc gcg gcg ctg cgg cag cag acg tgc ccg cgg tcc 732
195 Ile Asn Ala Ser Phe Ala Ala Leu Arg Gln Gln Thr Cys Pro Arg Ser
196      210      215      220
198 ggc ggc gac ggc aac ctg gcg ccc atc gac gtg cag acg ccg gtg agg 780
199 Gly Gly Asp Gly Asn Leu Ala Pro Ile Asp Val Gln Thr Pro Val Arg
200      225      230      235
202 ttc gac acg gcc tac ttc acc aac ctg ctg tcg cgg cgg ggc ctg ttc 828
203 Phe Asp Thr Ala Tyr Phe Thr Asn Leu Leu Ser Arg Arg Gly Leu Phe
204      240      245      250
206 cac tcg gac cag gag ctc ttc aac ggc ggg tcg cag gac gcg ctg gtg 876
207 His Ser Asp Gln Glu Leu Phe Asn Gly Gly Ser Gln Asp Ala Leu Val
208 255      260      265      270
210 agg cag tac agc gcc agc gcc tcg ctc ttc aac gcc gac ttc gtg gca 924
211 Arg Gln Tyr Ser Ala Ser Ala Ser Leu Phe Asn Ala Asp Phe Val Ala
212      275      280      285
214 gcc atg att agg atg ggc aac gtt ggg gtg ctc acc ggc acc gcc gga 972
215 Ala Met Ile Arg Met Gly Asn Val Gly Val Leu Thr Gly Thr Ala Gly
216      290      295      300
218 cag atc agg cgc aac tgc cgg gtc gtc aac agc tag atacgacgca 1018
219 Gln Ile Arg Arg Asn Cys Arg Val Val Asn Ser *
220      305      310
222 tcggattcga tcgatatact tgtagctata gctagcttgc tcgtcgaccg agcgcacatt 1078
223 gatagatcga ccgacataga gctcgtttct gatgaacccc agtacgtgta ctctctagta 1138
224 tatatacata gatatagcta tagattgaac acgtcgtcaa taccagtaga ataagtgggtg 1198
225 aacgaccacg caaggagaag agtgatcgaa gcagtgtcac ttgggttaccg aaatgattca 1258
226 tctgacattt tcgtattgga ttttgaacgc aactatatat atatatatat acactgttga 1318
227 cacctttttc ggaaaaaaaa aaaaaaaaaa aaaaaa 1354
229 <210> SEQ ID NO: 4
230 <211> LENGTH: 313
231 <212> TYPE: PRT
232 <213> ORGANISM: Zea mays
234 <400> SEQUENCE: 4
235 Met Ala Ser Pro Thr Leu Met Gln Cys Leu Val Ala Val Ser Leu Leu
236 1      5      10      15
237 Ser Cys Val Ala His Ala Gln Leu Ser Pro Thr Phe Tyr Ala Ser Ser
238      20      25      30
239 Cys Pro Asn Leu Gln Ser Ile Val Arg Ala Ala Met Thr Gln Ala Val
240      35      40      45
241 Ala Ser Glu Gln Arg Met Gly Ala Ser Leu Leu Arg Leu Phe Phe His
242      50      55      60
243 Asp Cys Phe Val Gln Gly Cys Asp Gly Ser Ile Leu Leu Asp Ala Gly

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244 65          70          75          80
245 Gly Glu Lys Thr Ala Gly Pro Asn Leu Asn Ser Val Arg Gly Phe Glu
246          85          90          95
247 Val Ile Asp Thr Ile Lys Arg Asn Val Glu Ala Ala Cys Pro Gly Val
248          100          105          110
249 Val Ser Cys Ala Asp Ile Leu Ala Leu Ala Ala Arg Asp Gly Thr Asn
250          115          120          125
251 Leu Leu Gly Gly Pro Thr Trp Ser Val Pro Leu Gly Arg Arg Asp Ser
252          130          135          140
253 Thr Thr Ala Ser Ala Ser Leu Ala Asn Ser Asn Pro Pro Pro Pro Thr
254 145          150          155          160
255 Ala Ser Leu Gly Thr Leu Ile Ser Leu Phe Gly Arg Gln Gly Leu Ser
256          165          170          175
257 Pro Arg Asp Met Thr Ala Leu Ser Gly Ala His Thr Ile Gly Gln Ala
258          180          185          190
259 Arg Cys Thr Thr Phe Arg Gly Arg Ile Tyr Gly Asp Thr Asp Ile Asn
260          195          200          205
261 Ala Ser Phe Ala Ala Leu Arg Gln Gln Thr Cys Pro Arg Ser Gly Gly
262          210          215          220
263 Asp Gly Asn Leu Ala Pro Ile Asp Val Gln Thr Pro Val Arg Phe Asp
264 225          230          235          240
265 Thr Ala Tyr Phe Thr Asn Leu Leu Ser Arg Arg Gly Leu Phe His Ser
266          245          250          255
267 Asp Gln Glu Leu Phe Asn Gly Gly Ser Gln Asp Ala Leu Val Arg Gln
268          260          265          270
269 Tyr Ser Ala Ser Ala Ser Leu Phe Asn Ala Asp Phe Val Ala Ala Met
270          275          280          285
271 Ile Arg Met Gly Asn Val Gly Val Leu Thr Gly Thr Ala Gly Gln Ile
272          290          295          300
273 Arg Arg Asn Cys Arg Val Val Asn Ser
274 305          310
277 <210> SEQ ID NO: 5
278 <211> LENGTH: 1263
279 <212> TYPE: DNA
280 <213> ORGANISM: Zea mays
282 <220> FEATURE:
283 <221> NAME/KEY: CDS
284 <222> LOCATION: (29)...(1099)
286 <400> SEQUENCE: 5
287 aaattatatg caatcgcaag cgagcaga atg gcg agg tcc agt ggt agt aga      52
288          Met Ala Arg Ser Ser Gly Ser Arg
289          1          5
291 cca gtg gcc ctc gtg ctg ctg gcg ctg tgc gcc gcc gcc ctc tcg tcg      100
292 Pro Val Ala Leu Val Leu Leu Ala Leu Cys Ala Ala Leu Ser Ser
293          10          15          20
295 gcc acg gtg acc gtg aat gag ccc atc gcc aat ggc ctc tcc tgg agc      148
296 Ala Thr Val Thr Val Asn Glu Pro Ile Ala Asn Gly Leu Ser Trp Ser
297 25          30          35          40
299 ttc tac gac gtt tcc tgc ccg tcg gtg gag ggc atc gtg cgc tgg cac      196

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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date